32. (New) A method of diagnosing colorectal cancer comprising:

a) determining the expression of a gene at least 75% identical to SEQ ID NO:1 in a first sample of a first individual; and

(b) comparing the expression of said gene in the first sample to expression of said gene in a second sample; wherein said comparison is used to diagnose colorectal cancer.

33. (New) The method of claim 32, wherein said second sample is from said first individual.

34. (New) The method of claim 33, wherein said first sample is colorectal tissue.

35. (New) The method of claim 33, wherein said second sample is colorectal tissue.

36. (New) The method of claim 33, wherein said second sample is cancerous tissue.

37. (New) The method of claim 32, wherein said second sample is from a second individual.

38. (New) The method of claim 37, wherein said first sample is colorectal tissue.

39. (New) The method of claim 37, wherein said second sample is colorectal tissue.

40.   (New) The method of claim 37, wherein said second sample is cancerous tissue.

41.   (New) The method of claim 32, wherein said gene is SEQ ID NO:1.

42.   (New) The method of claim 32, wherein said expression is measured using a labeled nucleic acid probe.

43.   (New) The method of claim 32, wherein said expression is measured utilizing a biochip.

44.   (New) A method for determining the prognosis of an individual with colorectal cancer comprising determining the expression of a gene at least 75% identical to SEQ ID NO:1 in a sample, wherein the expression of the gene is used to determine the prognosis of the individual.

45.   (New) The method of claim 44, wherein said gene is SEQ ID NO:1.

46.   (New) The method of claim 44, wherein said expression is measured using a labeled nucleic acid probe.

47.   (New) The method of claim 44, wherein said expression is measured utilizing a biochip.